

030

#14



OIEP

## RAW SEQUENCE LISTING

DATE: 05/22/2003

PATENT APPLICATION: US/10/055,624B

TIME: 11:27:49

Input Set : A:\sequence listing 10-055,624 created 05-07-2003.txt

Output Set: N:\CRF4\05222003\J055624B.raw

3 <110> APPLICANT: Adams, Sean H  
 4 Chui, Clarissa  
 5 Goddard, Audrey D  
 6 Grimaldi, J. Christopher  
 8 <120> TITLE OF INVENTION: BFIT COMPOSITIONS AND METHODS OF USE  
 10 <130> FILE REFERENCE: 9800081-0066  
 12 <140> CURRENT APPLICATION NUMBER: 10/055,624B  
 13 <141> CURRENT FILING DATE: 2002-01-22  
 15 <150> PRIOR APPLICATION NUMBER: US 60/263,362  
 16 <151> PRIOR FILING DATE: 2002-01-22  
 18 <160> NUMBER OF SEQ ID NOS: 23  
 20 <170> SOFTWARE: PatentIn version 3.2  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 1857  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Homo sapiens  
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 32 atggcagacg gcgagggata ccggaacccc acggaggtgc agatgagcca gctggtgctg 180  
 34 ccctgccaca ccaaccaacg tggtagctg agcgtcgggc agctgctcaa gtggattgac 240  
 36 accacggctt gcctgtccgc ggagaggcac gctggctgcc cctgtgtcac agcttccatg 300  
 38 gatgacatct attttgagca caccattagt gttggacaag tggtagaatat caaggccaag 360  
 40 gtgaaccggg ctttcaactc cagcatggag gtgggcatcc aggtggcctc ggaggacctg 420  
 42 tgctctgaga agcagtggaa tgtgtgcaag gccttggcca cttcgtggc ccgccgagag 480  
 44 atcaccaagg tgaagctgaa gcagatcacg ccgcggacag aagaggagaa gatggagcac 540  
 46 agtgtggcgg ctgagcgcgg gcgcgatgccc cttgtctatg cagacaccat caaggacctc 600  
 48 ctggccaact gcgccattca gggcgatctg gagagcagag actgtagccg catggtgccg 660  
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 54 agccggctct gccgtgcca ccctacgctg aaggccattg aaatgttcca cttccgaggc 840  
 56 ccgtcccagg tcggcgaccg tctgtgtgctc aaagccatcg tgaacaatgc cttcaaacat 900  
 58 agcatggagg tggcggtgtg cgtggaggcc tatcgccagg aggtgagac ccaccggcgc 960  
 60 cacatcaaca gtgcctttat gacctttgtg gtccctggacg cagatgacca gccccagttg 1020  
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80 acacaccgag agacgccaga gtacagacgc ggagagaccc tctgctcagg cttctgcctc 1620
82 tggcgcgagg gggaccagct gaccaagtgc tgctgggtta gggctccct gactgagctg 1680
84 gtctcgcaaa gtggcttcta ttcctggggg ctogaatcca ggtcaaaggg tcgcaggagc 1740
86 gacggttga atggaaaact agctggagga cacctgagta ctcttaaagc aatccccgtg 1800
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92 <211> LENGTH: 607
93 <212> TYPE: PRT
94 <213> ORGANISM: Homo sapiens
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99 1 5 10 15
102 Phe Ser Asn Arg Thr Ser Arg Lys Ser Ala Leu Arg Ala Gly Asn Asp
103 20 25 30
106 Ser Ala Met Ala Asp Gly Glu Gly Tyr Arg Asn Pro Thr Glu Val Gln
107 35 40 45
110 Met Ser Gln Leu Val Leu Pro Cys His Thr Asn Gln Arg Gly Glu Leu
111 50 55 60
114 Ser Val Gly Gln Leu Leu Lys Trp Ile Asp Thr Thr Ala Cys Leu Ser
115 65 70 75 80
118 Ala Glu Arg His Ala Gly Cys Pro Cys Val Thr Ala Ser Met Asp Asp
119 85 90 95
122 Ile Tyr Phe Glu His Thr Ile Ser Val Gly Gln Val Val Asn Ile Lys
123 100 105 110
126 Ala Lys Val Asn Arg Ala Phe Asn Ser Ser Met Glu Val Gly Ile Gln
127 115 120 125
130 Val Ala Ser Glu Asp Leu Cys Ser Glu Lys Gln Trp Asn Val Cys Lys
131 130 135 140
134 Ala Leu Ala Thr Phe Val Ala Arg Arg Glu Ile Thr Lys Val Lys Leu
135 145 150 155 160
138 Lys Gln Ile Thr Pro Arg Thr Glu Glu Glu Lys Met Glu His Ser Val
139 165 170 175
142 Ala Ala Glu Arg Arg Arg Met Arg Leu Val Tyr Ala Asp Thr Ile Lys
143 180 185 190
146 Asp Leu Leu Ala Asn Cys Ala Ile Gln Gly Asp Leu Glu Ser Arg Asp
147 195 200 205
150 Cys Ser Arg Met Val Pro Ala Glu Lys Thr Arg Val Glu Ser Val Glu
151 210 215 220
154 Leu Val Leu Pro Pro His Ala Asn His Gln Gly Asn Thr Phe Gly Gly
155 225 230 235 240
158 Gln Ile Met Ala Trp Met Glu Asn Val Ala Thr Ile Ala Ala Ser Arg
159 245 250 255
162 Leu Cys Arg Ala His Pro Thr Leu Lys Ala Ile Glu Met Phe His Phe
163 260 265 270
166 Arg Gly Pro Ser Gln Val Gly Asp Arg Leu Val Leu Lys Ala Ile Val
167 275 280 285
170 Asn Asn Ala Phe Lys His Ser Met Glu Val Gly Val Cys Val Glu Ala
171 290 295 300
174 Tyr Arg Gln Glu Ala Glu Thr His Arg Arg His Ile Asn Ser Ala Phe

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178 Met Thr Phe Val Val Leu Asp Ala Asp Asp Gln Pro Gln Leu Leu Pro
179          325          330          335
182 Trp Ile Arg Pro Gln Pro Gly Asp Gly Glu Arg Arg Tyr Arg Glu Ala
183          340          345          350
186 Ser Ala Arg Lys Lys Ile Arg Leu Asp Arg Lys Tyr Ile Val Ser Cys
187          355          360          365
190 Lys Gln Thr Glu Val Pro Leu Ser Val Pro Trp Asp Pro Ser Asn Gln
191          370          375          380
194 Val Tyr Leu Ser Tyr Asn Asn Val Ser Ser Leu Lys Met Leu Val Ala
195 385          390          395          400
198 Lys Asp Asn Trp Val Leu Ser Ser Glu Ile Ser Gln Val Arg Leu Tyr
199          405          410          415
202 Thr Leu Glu Asp Asp Lys Phe Leu Ser Phe His Met Glu Met Val Val
203          420          425          430
206 His Val Asp Ala Ala Gln Ala Phe Leu Leu Leu Ser Asp Leu Arg Gln
207          435          440          445
210 Arg Pro Glu Trp Asp Lys His Tyr Arg Ser Val Glu Leu Val Gln Gln
211          450          455          460
214 Val Asp Glu Asp Asp Ala Ile Tyr His Val Thr Ser Pro Ala Leu Gly
215 465          470          475          480
218 Gly His Thr Lys Pro Gln Asp Phe Val Ile Leu Ala Ser Arg Arg Lys
219          485          490          495
222 Pro Cys Asp Asn Gly Asp Pro Tyr Val Ile Ala Leu Arg Ser Val Thr
223          500          505          510
226 Leu Pro Thr His Arg Glu Thr Pro Glu Tyr Arg Arg Gly Glu Thr Leu
227          515          520          525
230 Cys Ser Gly Phe Cys Leu Trp Arg Glu Gly Asp Gln Leu Thr Lys Cys
231          530          535          540
234 Cys Trp Val Arg Val Ser Leu Thr Glu Leu Val Ser Ala Ser Gly Phe
235 545          550          555          560
238 Tyr Ser Trp Gly Leu Glu Ser Arg Ser Lys Gly Arg Arg Ser Asp Gly
239          565          570          575
242 Trp Asn Gly Lys Leu Ala Gly Gly His Leu Ser Thr Leu Lys Ala Ile
243          580          585          590
246 Pro Val Ala Lys Ile Asn Ser Arg Phe Gly Tyr Leu Gln Asp Thr
247          595          600          605
250 <210> SEQ ID NO: 3
251 <211> LENGTH: 1818
252 <212> TYPE: DNA
253 <213> ORGANISM: Homo sapiens
255 <400> SEQUENCE: 3
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258 ggctctgtg ttctccaacc gcacatcccg gaagtcagcc ttacgtgcgg ggaacgacag 120
260 tgccatggca gacggcgagg gataccggaa cccacggag gtgcagatga gccagctggt 180
262 gctgccctgc cacaccaacc aacgtggtga gctgagcgtc gggcagctgc tcaagtggat 240
264 tgacaccacg gcttgctgt ccgcggagag gcacgctggc tgcccctgtg tcacagcttc 300
266 catggatgac atctattttg agcacaccat tagtggtgga caagtgggga atatcaaggc 360
268 caaggtgaac cgggccttca actccagcat ggaggtgggc atccaggtgg cctcggagga 420

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270 cctgtgctct gagaagcagt ggaatgtgtg caaggccttg gccaccttcg tggcccgccg      480
272 agagatcacc aaggtgaagc tgaagcagat cacgccgcgg acagaagagg agaagatgga      540
274 gcacagtgtg gcggctgagc gccggcgcat gcgccttgtc tatgcagaca ccatcaagga      600
276 cctcctggcc aactgcgcca ttcagggcga tctggagagc agagactgta gccgcatggt      660
278 gccggctgag aagacccgtg tggagagtgt ggagctggtc ctgcctcccc acgccaatca      720
280 ccagggcaac acctttgggg gccagatcat ggcttgatg gagaatgtgg ccaccattgc      780
282 agccagccgg ctctgccgtg cccaccctac gctgaaggcc attgaaatgt tccacttccg      840
284 aggccgtcc caggtcggcg accgtctggt gctcaaagcc atcgtgaaca atgccttcaa      900
286 acatagcatg gaggtgggcg tgtgcgtgga ggctatcgc caggaggctg agacccaccg      960
288 gcgccacatc aacagtgcct ttatgacctt tgtggtcctg gacgcagatg accagcccca     1020
290 gttgctgccc tggattcggc cccagcccg gcgtggtag cggcggtacc gagaggccag     1080
292 tgccagaaag aagatccgcc tggacaggaa gtacatcgtg tcctgtaagc agacagagggt     1140
294 gcccctctcc gtcccctggg accctagcaa ccagggtgtac ctgagctaca ataacgtctc     1200
296 ctcttggaag atgcttgtgg ccaaggacaa ctgggtgctg tcctcggaag tcagtcagggt     1260
298 ccgcctgtac actctggagg atgacaagtt cctctccttc cacatggaga tgggtggtgca     1320
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302 caagcactac cggagcgtgg agctagtgca gcaggtagac gaggacgacg ccatctacca     1440
304 cgtcaccagc cctgcctcgt gaggtcacac aaagccccag gacttcgtga tcctggcctc     1500
306 gaggcggaag ccttgtgaca atggggaccc ctatgtcatc gcgctgagggt cggtcacgct     1560
308 gcccacacac cgagagacgc cagagtacag acgcggagag accctctgct caggcttctg     1620
310 cctctggcgc gaggggggacc agctgaccaa ggtatcctac tacaaccagg ccaccccagg     1680
312 tgttctcaac tatgtgacca ccaacgtggc cggcctctcc tctgagttct acaccacctt     1740
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316 cctctagatg ccctcagc                                     1818
319 <210> SEQ ID NO: 4
320 <211> LENGTH: 594
321 <212> TYPE: PRT
322 <213> ORGANISM: Homo sapiens
324 <400> SEQUENCE: 4
326 Met Ile Gln Asn Val Gly Asn His Leu Arg Arg Gly Leu Ala Ser Val
327 1 5 10 15
330 Phe Ser Asn Arg Thr Ser Arg Lys Ser Ala Leu Arg Ala Gly Asn Asp
331 20 25 30
334 Ser Ala Met Ala Asp Gly Glu Gly Tyr Arg Asn Pro Thr Glu Val Gln
335 35 40 45
338 Met Ser Gln Leu Val Leu Pro Cys His Thr Asn Gln Arg Gly Glu Leu
339 50 55 60
342 Ser Val Gly Gln Leu Leu Lys Trp Ile Asp Thr Thr Ala Cys Leu Ser
343 65 70 75 80
346 Ala Glu Arg His Ala Gly Cys Pro Cys Val Thr Ala Ser Met Asp Asp
347 85 90 95
350 Ile Tyr Phe Glu His Thr Ile Ser Val Gly Gln Val Val Asn Ile Lys
351 100 105 110
354 Ala Lys Val Asn Arg Ala Phe Asn Ser Ser Met Glu Val Gly Ile Gln
355 115 120 125
358 Val Ala Ser Glu Asp Leu Cys Ser Glu Lys Gln Trp Asn Val Cys Lys
359 130 135 140
362 Ala Leu Ala Thr Phe Val Ala Arg Arg Glu Ile Thr Lys Val Lys Leu
363 145 150 155 160

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366 Lys Gln Ile Thr Pro Arg Thr Glu Glu Glu Lys Met Glu His Ser Val
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370 Ala Ala Glu Arg Arg Arg Met Arg Leu Val Tyr Ala Asp Thr Ile Lys
371          180          185          190
374 Asp Leu Leu Ala Asn Cys Ala Ile Gln Gly Asp Leu Glu Ser Arg Asp
375          195          200          205
378 Cys Ser Arg Met Val Pro Ala Glu Lys Thr Arg Val Glu Ser Val Glu
379          210          215          220
382 Leu Val Leu Pro Pro His Ala Asn His Gln Gly Asn Thr Phe Gly Gly
383 225          230          235          240
386 Gln Ile Met Ala Trp Met Glu Asn Val Ala Thr Ile Ala Ala Ser Arg
387          245          250          255
390 Leu Cys Arg Ala His Pro Thr Leu Lys Ala Ile Glu Met Phe His Phe
391          260          265          270
394 Arg Gly Pro Ser Gln Val Gly Asp Arg Leu Val Leu Lys Ala Ile Val
395          275          280          285
398 Asn Asn Ala Phe Lys His Ser Met Glu Val Gly Val Cys Val Glu Ala
399          290          295          300
402 Tyr Arg Gln Glu Ala Glu Thr His Arg Arg His Ile Asn Ser Ala Phe
403 305          310          315          320
406 Met Thr Phe Val Val Leu Asp Ala Asp Asp Gln Pro Gln Leu Leu Pro
407          325          330          335
410 Trp Ile Arg Pro Gln Pro Gly Asp Gly Glu Arg Arg Tyr Arg Glu Ala
411          340          345          350
414 Ser Ala Arg Lys Lys Ile Arg Leu Asp Arg Lys Tyr Ile Val Ser Cys
415          355          360          365
418 Lys Gln Thr Glu Val Pro Leu Ser Val Pro Trp Asp Pro Ser Asn Gln
419          370          375          380
422 Val Tyr Leu Ser Tyr Asn Asn Val Ser Ser Leu Lys Met Leu Val Ala
423 385          390          395          400
426 Lys Asp Asn Trp Val Leu Ser Ser Glu Ile Ser Gln Val Arg Leu Tyr
427          405          410          415
430 Thr Leu Glu Asp Asp Lys Phe Leu Ser Phe His Met Glu Met Val Val
431          420          425          430
434 His Val Asp Ala Ala Gln Ala Phe Leu Leu Leu Ser Asp Leu Arg Gln
435          435          440          445
438 Arg Pro Glu Trp Asp Lys His Tyr Arg Ser Val Glu Leu Val Gln Gln
439          450          455          460
442 Val Asp Glu Asp Asp Ala Ile Tyr His Val Thr Ser Pro Ala Leu Gly
443 465          470          475          480
446 Gly His Thr Lys Pro Gln Asp Phe Val Ile Leu Ala Ser Arg Arg Lys
447          485          490          495
450 Pro Cys Asp Asn Gly Asp Pro Tyr Val Ile Ala Leu Arg Ser Val Thr
451          500          505          510
454 Leu Pro Thr His Arg Glu Thr Pro Glu Tyr Arg Arg Gly Glu Thr Leu
455          515          520          525
458 Cys Ser Gly Phe Cys Leu Trp Arg Glu Gly Asp Gln Leu Thr Lys Val
459          530          535          540
462 Ser Tyr Tyr Asn Gln Ala Thr Pro Gly Val Leu Asn Tyr Val Thr Thr

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**VERIFICATION SUMMARY**

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